

What is claimed is:

1. A polypeptide chain useful as a subunit of a dimeric osteogenic protein comprising a pair of disulfide-bonded polypeptide chains,

said polypeptide chain having an amino acid sequence sufficiently duplicative of Sequence ID No. 1 or Sequence ID No. 3 such that the dimeric osteogenic protein comprising said polypeptide chain has a conformation capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix.

2. The polypeptide chain of claim 1 wherein the sequence comprises (Sequence ID No. 1):

mOP-2

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Ieu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
	30						35	
Val	Cys	Arg	Arg	His	Glu	Ieu	Tyr	Val
			40					45
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
	55				60			

Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
			65			70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			75				80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
			120				125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His.					

3. The polypeptide chain of claim 1 wherein the sequence comprises (Sequence ID No. 3):

hOP-2

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45

Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
110						115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His.					

4. The polypeptide chain of claim 1 wherein the sequence comprises (Sequence ID No. 7):

Cys	Xaa									
	1				5				10	
Xaa										
					15				20	
Xaa	Cys	Xaa	Xaa	Xaa						
					25				30	
Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa
					35				40	

Xaa  
45 50 55

Xaa Cys  
60 65

Cys Xaa  
70 75

Xaa  
80 85

Xaa Cys  
90 95

Xaa Cys Xaa  
100

and wherein each Xaa independently represents one of the 20 naturally occurring L-isomer,  $\alpha$ -amino acids, and together with said 8 cysteine residues define said polypeptide chain.

5. The polypeptide chain of claim 1 wherein the sequence comprises (Sequence ID No. 8):

Xaa  
1 5 10

Xaa  
15 20

Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa  
25 30

Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40

Xaa  
45 50 55

Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa  
60 65

Xaa											
					70					75	
Xaa											
					80					85	
Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys	Xaa			
					90				95		

wherein each Xaa independently represents one of the 20 naturally occurring L-isomer,  $\alpha$ -amino acids, and together with said 7 cysteine residues define said polypeptide chain.

6. A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix; said polypeptide chain comprising the amino acid sequence (Sequence ID No. 5):

Cys	Xaa <sub>1</sub>	Xaa <sub>2</sub>	His	Glu	Leu	Tyr	Val	Xaa <sub>3</sub>	Phe		
	1			5						10	
Xaa <sub>4</sub>	Asp	Leu	Gly	Trp	Xaa <sub>5</sub>	Asp	Trp	Xaa <sub>6</sub>	Ile		
					15				20		
Ala	Pro	Xaa <sub>7</sub>	Gly	Tyr	Xaa <sub>8</sub>	Ala	Tyr	Tyr	Cys		
					25				30		
Glu	Gly	Cys	Xaa <sub>9</sub>	Phe	Pro	Leu	Xaa <sub>10</sub>	Ser	Xaa <sub>11</sub>		
				35					40		
Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Xaa <sub>12</sub>	Thr		
					45				50		
Leu	Xaa <sub>13</sub>	Xaa <sub>14</sub>	Xaa <sub>15</sub>	Xaa <sub>16</sub>	Xaa <sub>17</sub>	Xaa <sub>18</sub>	Val				
					55						
Pro	Lys	Xaa <sub>19</sub>	Cys	Cys	Ala	Pro	Thr	Xaa <sub>20</sub>	Leu		
					60				65		

Xaa <sub>21</sub>	Ala	Xaa <sub>22</sub>	Ser	Val	Leu	Tyr	Xaa <sub>23</sub>	Asp	
			70				75		
Xaa <sub>24</sub>	Ser	Xaa <sub>25</sub>	Asn	Val	Xaa <sub>26</sub>	Leu	Xaa <sub>27</sub>	Lys	
			80				85		
Xaa <sub>28</sub>	Pro	Asn	Met	Val	Val	Xaa <sub>29</sub>	Ala	Cys	Gly
			90				95		

Cys His,

wherein Xaa<sub>1</sub> = (Lys or Arg); Xaa<sub>2</sub> = (Lys or Arg); Xaa<sub>3</sub> = (Ser or Arg); Xaa<sub>4</sub> = (Arg or Gln); Xaa<sub>5</sub> = (Gln or Leu); Xaa<sub>6</sub> = (Ile or Val); Xaa<sub>7</sub> = (Glu or Gln); Xaa<sub>8</sub> = (Ala or Ser); Xaa<sub>9</sub> = (Ala or Ser); Xaa<sub>10</sub> = (Asn or Asp); Xaa<sub>11</sub> = (Tyr or Cys); Xaa<sub>12</sub> = (Val or Leu); Xaa<sub>13</sub> = (His or Asn); Xaa<sub>14</sub> = (Phe or Leu); Xaa<sub>15</sub> = (Ile or Met); Xaa<sub>16</sub> = (Asn or Lys); Xaa<sub>17</sub> = (Glu, Asp or Asn); Xaa<sub>18</sub> = (Thr, Ala or Val); Xaa<sub>19</sub> = (Pro or Ala); Xaa<sub>20</sub> = (Gln or Lys); Xaa<sub>21</sub> = (Asn or Ser); Xaa<sub>22</sub> = (Ile or Thr); Xaa<sub>23</sub> = (Phe or Tyr); Xaa<sub>24</sub> = (Asp, Glu or Ser); Xaa<sub>25</sub> = (Ser or Asn); Xaa<sub>26</sub> = (Ile or Asp); Xaa<sub>27</sub> = (Lys or Arg); Xaa<sub>28</sub> = (Tyr, Ala or His); and Xaa<sub>29</sub> = (Arg or Lys).

7. The polypeptide chain of claim 6 wherein Xaa<sub>11</sub> = Cys.

8. A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix; the amino acid sequence of said polypeptide chain being at least 70% homologous with the amino acid sequence (Sequence ID No. 1):

mOP-2

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His.					

9. The polypeptide chain of claim 8 wherein the amino acid sequence is at least 80% homologous with the amino acid sequence (Sequence ID No. 1):

mOP-2

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120						125

Lys His Arg Asn Met Val Val Lys Ala  
130 135  
Cys Gly Cys His.

10. The polypeptide chain of claim 8 wherein the amino acid sequence comprises (Sequence ID No. 1):

mOP-2

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
	30						35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
		40						45
Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			

Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
	120					125		
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130				135	
Cys	Gly	Cys	His.					

11. The polypeptide chain of claim 8 wherein the amino acid sequence comprises (Sequence ID No. 3):

hOP-2

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
	30						35	
Val	Cys	Arg	Arg	His	Glu	Ieu	Tyr	Val
		40						45
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90

Val	His	Leu	Met	Lys 95	Pro	Asn	Ala	Val
Pro 100	Lys	Ala	Cys	Cys	Ala 105	Pro	Thr	Lys
Leu 110	Ser	Ala	Thr	Ser	Val	Leu 115	Tyr	Tyr
Asp 120	Glu	Ser	Asn	Asn	Val	Ile	Leu 125	Arg
Lys 130	Ala	Arg	Asn	Met	Val	Val	Lys 135	Ala
Cys	Gly	Cys	His.					

12. The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 9):

hOP-2P

			Pro 1	Leu	Arg	Arg	Arg	Gln 5
Pro	Lys	Lys	Ser 10	Asn	Glu	Leu	Pro	Gln 15
Ala	Asn	Arg	Leu	Pro 20	Gly	Ile	Phe	Asp
Asp 25	Val	Asn	Gly	Ser	His 30	Gly	Arg	Gln
Val 35	Cys	Arg	Arg	His	Glu	Leu 40	Tyr	Val
Ser	Phe	Gln 45	Asp	Leu	Gly	Trp	Leu	Asp
Tyr	Val	Ile 55	Ala	Pro	Gln	Gly	Tyr	Ser 60
Ala	Tyr	Tyr	Cys 65	Glu	Gly	Glu	Cys	Ser

Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
70					75			
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
	80					85		
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
		90					95	
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
			100					105
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
				110				
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
115					120			
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
		125					130	
Cys	Gly	Cys	His.					
			135					

13. The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 10):

hOP-2R

						Arg	Arg	Gln
						1		
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
	5					10		
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
		15					20	
Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
			25					30
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
				35				

Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
40					45			
Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
	50					55		
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
		60					65	
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			70					75
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
				80				
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
	85				90			
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
	95					100		
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		105					110	
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
			115					120
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
				125				
Cys	Gly	Cys	His.					
	130							

14. The polypeptide chain of claim 8 wherein the amino acid sequence comprises (SEQ ID NO. 11):

hOP-2S

					Ser	Gln	Gln	
					1			
Pro	Phe	Val	Val	Thr	Phe	Phe	Arg	Ala
		5				10		
Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg
			15				20	

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
			25					30
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
				35				
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
40					45			
Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
	50					55		
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
		60					65	
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
			70					75
Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
				80				
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
85					90			
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
	95					100		
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
		105					110	
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
			115					120
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
				125				
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
130					135			
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
		140				145		
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
			150				165	
Cys	Gly	Cys	His.					
			170					

15. A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix; said polypeptide chain having an amino acid sequence comprising (Sequence ID No. 2):

Prepro mOP-2

	Met	Ala	Met	Arg	Pro	Gly	Pro	Leu	
	1				5				
Trp	Leu	Leu	Gly	Leu	Ala	Leu	Cys	Ala	
	10					15			
Leu	Gly	Gly	Gly	His	Gly	Pro	Gly	Pro	
		20					25		
Pro	His	Thr	Cys	Pro	Gln	Arg	Arg	Leu	
			30					35	
Gly	Ala	Arg	Asp	Arg	Asp	Met	Gln	Arg	
				40					
Glu	Ile	Leu	Ala	Val	Leu	Gly	Leu	Pro	
	45				50				
Gly	Arg	Pro	Asp	Pro	Val	His	Asn	Pro	
	55					50			
Pro	Leu	Pro	Gly	Thr	Gln	Arg	Ala	Pro	
		65				70			
Leu	Phe	Met	Leu	Asp	Leu	Tyr	His	Ala	
			70				80		
Met	Thr	Asp	Asp	Asp	Asp	Gly	Gly	Pro	
				85					
Pro	Gln	Ala	His	Leu	Gly	Arg	Ala	Asp	
	90				95				
Leu	Val	Met	Ser	Phe	Val	Asn	Met	Val	
		100				105			

Glu	Arg	Asp	Arg	Thr	Leu	Gly	Tyr	Gln
		110				115		
Glu	Pro	His	Trp	Lys	Glu	Phe	His	Phe
			120					125
Asp	Leu	Thr	Gln	Ile	Pro	Ala	Gly	Glu
				130				
Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile
135					140			
Tyr	Lys	Glu	Pro	Ser	Thr	His	Pro	Leu
145						150		
Asn	Thr	Thr	Leu	His	Ile	Ser	Met	Phe
		155					160	
Glu	Val	Val	Gln	Glu	His	Ser	Asn	Arg
			165					170
Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	Leu
				175				
Gln	Thr	Leu	Arg	Ser	Gly	Asp	Glu	Gly
180					185			
Trp	Leu	Val	Leu	Asp	Ile	Thr	Ala	Ala
190						195		
Ser	Asp	Arg	Trp	Leu	Leu	Asn	His	His
		200					205	
Lys	Asp	Leu	Gly	Leu	Arg	Leu	Tyr	Val
			210					215
Glu	Thr	Ala	Asp	Gly	His	Ser	Met	Asp
				220				
Pro	Gly	Leu	Ala	Gly	Leu	Leu	Gly	Arg
225					230			
Gln	Ala	Pro	Arg	Ser	Arg	Gln	Pro	Phe
235						240		
Met	Val	Thr	Phe	Phe	Arg	Ala	Ser	Gln
		245						250
Ser	Pro	Val	Arg	Ala	Pro	Arg	Ala	Ala
			255					260

Arg	Pro	Leu	Lys	Arg 265	Arg	Gln	Pro	Lys
Lys 270	Thr	Asn	Glu	Leu	Pro 275	His	Pro	Asn
Lys 280	Leu	Pro	Gly	Ile	Phe	Asp 285	Asp	Gly
His 290	Gly	Ser	Arg	Gly	Arg	Glu	Val 295	Cys
Arg 300	Arg	His	Glu	Leu	Tyr	Val	Arg 305	Phe
Arg 310	Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val
Ile 315	Ala	Pro	Gln	Gly	Tyr 320	Ser	Ala	Tyr
Tyr 325	Cys	Glu	Gly	Glu	Cys	Aia 330	Phe	Pro
Leu 335	Asp	Ser	Cys	Met	Asn	Ala	Thr 340	Asn
His 345	Ala	Ile	Leu	Gln	Ser	Leu	Val 350	His
Leu 355	Met	Lys	Pro	Asp	Val	Val	Pro	Lys
Ala 360	Cys	Cys	Ala	Pro	Thr 365	Lys	Leu	Ser
Ala 370	Thr	Ser	Val	Leu	Tyr	Tyr 375	Asp	Ser
Ser 380	Asn	Asn	Val	Ile	Leu	Arg	Lys 385	His
Arg 390	Asn	Met	Val	Val	Lys	Ala	Cys 395	Gly
Cys	His.							

16. A polypeptide chain useful as a subunit of a dimeric osteogenic protein, said protein being

capable of inducing endochondral bone formation when implanted in a mammal in association with a matrix; said polypeptide chain comprising the amino acid sequence (Sequence ID No. 4):

Prepro hOP-2

Met	Thr	Ala	Leu	Pro	Gly	Pro	Leu	Trp
1				5				
Leu	Leu	Gly	Leu	Ala	Leu	Cys	Ala	Leu
10					15			
Gly	Gly	Gly	Gly	Pro	Gly	Leu	Arg	Pro
20						25		
Pro	Pro	Gly	Cys	Pro	Gln	Arg	Arg	Leu
			30				35	
Gly	Ala	Arg	Asp	Arg	Asp	Val	Gln	Arg
			40					45
Glu	Ile	Leu	Ala	Val	Leu	Gly	Leu	Pro
				50				
Gly	Arg	Pro	Arg	Pro	Arg	Ala	Pro	Pro
55					60			
Ala	Ala	Ser	Arg	Leu	Pro	Ala	Ser	Ala
		65				70		
Pro	Leu	Phe	Met	Leu	Asp	Leu	Tyr	His
		75					80	
Arg	Met	Ala	Gly	Asp	Asp	Asp	Glu	Asp
			85					90
Gly	Ala	Ala	Glu	Ala	Leu	Gly	Arg	Ala
				95				
Asp	Leu	Val	Met	Ser	Phe	Val	Asn	Met
100					105			
Val	Glu	Arg	Asp	Arg	Ala	Leu	Gly	His
		110					115	

Gln	Glu	Pro	His	Trp	Lys	Glu	Phe	Arg
		120					125	
Phe	Asp	Leu	Thr	Gln	Ile	Pro	Ala	Gly
			130					135
Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg
				140				
Ile	Tyr	Lys	Val	Pro	Ser	Ile	His	Leu
145					150			
Leu	Asn	Arg	Thr	Leu	His	Val	Ser	Met
		155				160		
Phe	Gln	Val	Val	Gln	Glu	Gln	Ser	Asn
		165					170	
Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp
		175						180
Leu	Gln	Thr	Leu	Arg	Ala	Gly	Asp	Glu
				185				
Gly	Trp	Leu	Val	Leu	Asp	Val	Thr	Ala
190					195			
Ala	Ser	Asp	Cys	Trp	Leu	Leu	Lys	Arg
	200					205		
His	Lys	Asp	Leu	Gly	Leu	Arg	Leu	Tyr
		210					215	
Val	Glu	Thr	Glu	Asp	Gly	His	Ser	Val
			220					225
Asp	Pro	Gly	Leu	Ala	Gly	Leu	Leu	Gly
				230				
Gln	Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro
235					240			
Phe	Val	Val	Thr	Phe	Phe	Arg	Ala	Ser
	245					250		
Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg	Ala
		255						260

Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln	Pro
			265					270
Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln	Ala
				275				
Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp	Asp
280					285			
Val	His	Gly	Ser	His	Gly	Arg	Gln	Val
	290					295		
Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser
	300						305	
Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp	Trp
	310							315
Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala
				320				
Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser	Phe
325					330			
Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala	Thr
	335					340		
Asn	His	Ala	Ile	Leu	Gln	Ser	Leu	Val
	345						350	
His	Leu	Met	Lys	Pro	Asn	Ala	Val	Pro
			355					360
Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu
				365				
Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr	Asp
370					375			
Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys
	380					385		
Ala	Arg	Asn	Met	Val	Val	Lys	Ala	Cys
	390						395	
Gly	Cys	His.						

17. A dimeric osteogenic protein capable of inducing endochondral bone formation in a mammal when

implanted in said mammal in association with a matrix; said protein comprising a pair of disulfide-bonded polypeptide chains constituting a dimeric species, wherein each said polypeptide chain is the polypeptide chain of claim 1, 6, 8, 15 or 16.

18. The polypeptide chain of claim 1, 6, 8, 15 or 16 produced by expression of recombinant DNA in a host cell.

19. The polypeptide chain of claim 15 wherein said host cell is a procaryotic host cell.

20. The polypeptide chain of claim 15 wherein said host cell is a mammalian cell.

21. The polypeptide of claim 1, 6, 8, 15 or 16 that is glycosylated.

22. A DNA encoding the polypeptide chain of claim 1, 6, 8, 15 or 16.

23. A dimeric protein comprising a pair of polypeptide chains expressed from a DNA sequence sufficiently duplicative of the sequence of Sequence ID No. 2 or Sequence ID No. 4 such that, when said polypeptide chains are oxidized to produce a disulfide-bonded dimeric species, the dimeric species has a conformation that is capable of inducing endochondral bone or cartilage formation when disposed within a matrix and implanted in a mammal.